



IFWO

RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/797,248A

TIME: 11:12:33

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\08262004\J797248A.raw

3 <110> APPLICANT: Dumas, Renaud
 4 Lebrun, Marc-Henri
 5 Zundel, Jean-Luc
 6 Effantin, Geraldine
 7 Morin, Valerie
 9 <120> TITLE OF INVENTION: Use of inhibitors of ketol-acid reductoisomerase to prevent
 or treat

10 fungal infection of plants
 12 <130> FILE REFERENCE: A36156-PCT-USA-A 072667.0196
 14 <140> CURRENT APPLICATION NUMBER: 10/797,248A
 15 <141> CURRENT FILING DATE: 2004-03-10
 17 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: Custom
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 402
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Magnaporthe grisea
 26 <220> FEATURE:
 27 <221> NAME/KEY: TRANSIT
 28 <222> LOCATION: (1)..(51)
 29 <223> OTHER INFORMATION: Putative mitochondrial transit peptide
 31 <400> SEQUENCE: 1
 32 Met Ser Ala Arg Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln
 33 1 5 10 15
 35 Leu Ala Thr Pro Ala Val Gln Arg Arg Ser Phe Val Ala Ala Ser Ser
 36 20 25 30
 38 Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
 39 35 40 45
 41 Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
 42 50 55 60
 44 Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
 45 65 70 75 80
 47 Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
 48 85 90 95
 50 Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
 51 100 105 110
 53 Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
 54 115 120 125
 56 Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
 57 130 135 140
 59 Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala
 60 145 150 155 160
 62 Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly
 63 165 170 175

(pg.6)
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65 Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp
66          180          185          190
68 Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
69          195          200          205
71 Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
72          210          215          220
74 Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
75 225          230          235          240
77 Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val
78          245          250          255
80 Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
81          260          265          270
83 Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
84          275          280          285
86 Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu
87          290          295          300
89 Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys
90 305          310          315          320
92 Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys
93          325          330          335
95 Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
96          340          345          350
98 Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
99          355          360          365
101 Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile
102          370          375          380
104 Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
105 385          390          395          400
107 Gln Lys
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 395
113 <212> TYPE: PRT
114 <213> ORGANISM: Saccharomyces cerevisiae
116 <220> FEATURE:
117 <221> NAME/KEY: TRANSIT
118 <222> LOCATION: (1)..(47)
119 <223> OTHER INFORMATION: mitochondrial transit peptide
121 <300> PUBLICATION INFORMATION:
122 <308> DATABASE ACCESSION NO: gb:X04969
123 <309> DATABASE ENTRY DATE: 1993-09-12
125 <400> SEQUENCE: 2
126 Met Leu Arg Thr Gln Ala Ala Arg Leu Ile Cys Asn Ser Arg Val Ile
127 1          5          10          15
130 Thr Ala Lys Arg Thr Phe Ala Leu Ala Thr Arg Ala Ala Ala Tyr Ser
131          20          25          30
133 Arg Pro Ala Ala Arg Phe Val Lys Pro Met Ile Thr Thr Arg Gly Leu
134          35          40          45
136 Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
137          50          55          60

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139 Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
140 65 70 75 80
142 Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
143 85 90 95
145 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
146 100 105 110
148 Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
149 115 120 125
151 Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
152 130 135 140
154 Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
155 145 150 155 160
157 Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
158 165 170 175
160 Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
161 180 185 190
163 Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
164 195 200 205
166 Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
167 210 215 220
169 Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
170 225 230 235 240
172 Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
173 245 250 255
175 Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
176 260 265 270
178 Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
179 275 280 285
181 Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
182 290 295 300
184 Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
185 305 310 315 320
187 Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
188 325 330 335
190 Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
191 340 345 350
193 Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
194 355 360 365
196 Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
197 370 375 380
199 Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
200 385 390 395
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 400
205 <212> TYPE: PRT
206 <213> ORGANISM: Neurospora crassa
208 <220> FEATURE:
209 <221> NAME/KEY: TRANSIT
210 <222> LOCATION: (1)..(53)

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211 <223> OTHER INFORMATION: putative mitochondrial transit peptide

213 <300> PUBLICATION INFORMATION:

214 <308> DATABASE ACCESSION NO: gb:M84189.1

215 <309> DATABASE ENTRY DATE: 1996-05-23

217 <400> SEQUENCE: 3

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219   1           5           10           15
221 Leu Ala Thr Pro Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ala Ser
222           20           25           30
224 Ala Val Arg Ala Ser Val Ala Val Lys Ala Val Ala Ala Pro Ala Arg
225           35           40           45
227 Gln Gln Val Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu
228           50           55           60
230 Glu Val His Glu Arg Ala Asp Trp Pro Ala Glu Lys Leu Leu Asp Tyr
231   65           70           75           80
233 Phe Lys Asn Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His
234           85           90           95
236 Gly Gln Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Val Gly
237           100          105          110
239 Val Arg Lys Asn Gly Lys Ser Trp Glu Asp Ala Ile Gln Asp Gly Trp
240           115          120          125
242 Val Pro Gly Lys Asn Leu Phe Asp Val Asp Glu Ala Ile Ser Arg Gly
243           130          135          140
245 Thr Ile Val Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp
246 145           150          155          160
248 Pro His Ile Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser
249           165          170          175
251 His Gly Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro
252           180          185          190
254 Thr Asp Val Asp Val Ile Leu Val Ala Pro Lys Gly Ser Gly Arg Thr
255           195          200          205
257 Val Arg Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala
258           210          215          220
260 Val Tyr Gln Asp Val Thr Gly Lys Ala Lys Glu Lys Ala Val Ala Leu
261 225           230          235          240
263 Gly Val Ala Val Gly Ser Gly Tyr Leu Tyr Glu Thr Thr Phe Glu Lys
264           245          250          255
266 Glu Val Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly
267           260          265          270
269 Ile His Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly
270           275          280          285
272 His Ser Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln
273           290          295          300
275 Ser Leu Tyr Pro Leu Ile Gly Ala His Gly Met Asp Trp Met Phe Asp
276 305           310          315          320
278 Ala Cys Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Thr Pro Lys
279           325          330          335
281 Phe Lys Asp Ala Leu Lys Pro Val Phe Asn Asn Leu Tyr Asp Ser Val
282           340          345          350

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Input Set : A:\pto.lm.txt

Output Set : N:\CRF4\08262004\J797248A.raw

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284 Lys Asn Gly Asp Glu Arg Lys Arg Ser Leu Glu Tyr Asn Ser Gln Pro
285          355          360          365
287 Asp Tyr Arg Glu Arg Tyr Glu Ala Glu Leu Asp Glu Ile Arg Asn Leu
288          370          375          380
290 Glu Ile Trp Arg Ala Gly Lys Arg Ser Leu Arg Pro Glu Asn Gln Lys
291 385          390          395          400
297 <210> SEQ ID NO: 4
298 <211> LENGTH: 1356
299 <212> TYPE: DNA
300 <213> ORGANISM: Magnaporthe grisea
302 <220> FEATURE:
303 <221> NAME/KEY: 5'UTR
304 <222> LOCATION: (1)..(43)
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (44)..(1246)
310 <220> FEATURE:
311 <221> NAME/KEY: 3'UTR
312 <222> LOCATION: (1247)..(1356)
314 <220> FEATURE:
315 <221> NAME/KEY: polyA_site
316 <222> LOCATION: (1322)..(1330)
318 <400> SEQUENCE: 4
319 ttgtttttct tggttcctta ttctaccttg tcacacaaca aac atg tct gct cgc 55
320                               Met Ser Ala Arg
321                               1
323 ggt ttc tca aag gct ttg agg cca atg gcc cgc caa ttg gcc act ccc 103
324 Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln Leu Ala Thr Pro
325 5          10          15          20
327 gcc gtt cag agg cgt acc ttc gtg gct gct tct agc atg gtg cgg gcc 151
328 Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser Met Val Arg Ala
329          25          30          35
331 acc agg aaa gcc gcc gtc gct ccc act cag cag cag atc cgt ggt gtc 199
332 Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln Ile Arg Gly Val
333          40          45          50
335 aag acc atg gat ttt gct ggc cac aag gag cag gtc tgg gag cgt gcc 247
336 Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val Trp Glu Arg Ala
337          55          60          65
339 gac tgg ccc aag gag aag ctg ctg gag tac ttc aag gac gac acc ctt 295
340 Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys Asp Asp Thr Leu
341          70          75          80
343 gcc ctc atc ggc tat ggt tcg cag ggc cac ggc cag ggt ctt aac ctc 343
344 Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln Gly Leu Asn Leu
345 85          90          95          100
347 cgc gac aac ggc ctc aac gtc atc atc ggt gtg cgc aag gac gga aag 391
348 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Lys
349          105          110          115
351 tcg tgg aag gac gcc gtc cag gac ggc tgg gtt ccc ggc aag aac ctc 439
352 Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro Gly Lys Asn Leu

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/26/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 9,12
Seq#:9; N Pos. 6,12,15,18
Seq#:10; N Pos. 6,9,18

VERIFICATION SUMMARY

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\08262004\J797248A.raw

L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0